

SEQUENCE LISTING

<110> Isis Pharmaceuticals, Inc.
 National University of Singapore
 Monia, Brett P.
 Dobie, Kenneth W.
 Freier, Susan M.
 Popoff, Ian
 Wong, Wai Shiu Fred
 Karras, James G.

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 Activated Protein Kinase Expression

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<151> 2003-08-15

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gggtgcgggtg caggcggggg cccacagggg ccaccttctt gcccggcggc tgccgctgga 360
aa atg tct cag gag agg ccc acg ttc tac cgg cag gag ctg aac aag 407
Met Ser Gln Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys
      1             5             10             15

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aca atc tgg gag gtg ccc gag cgt tac cag aac ctg tct cca gtg ggc 455
Thr Ile Trp Glu Val Pro Glu Arg Tyr Gln Asn Leu Ser Pro Val Gly
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tct ggc gcc tat ggc tct gtg tgt gct gct ttt gac aca aaa acg ggg 503
Ser Gly Ala Tyr Gly Ser Val Cys Ala Ala Phe Asp Thr Lys Thr Gly
              35              40              45

```

```

tta cgt gtg gca gtg aag aag ctc tcc aga cca ttt cag tcc atc att 551
Leu Arg Val Ala Val Lys Lys Leu Ser Arg Pro Phe Gln Ser Ile Ile
              50              55              60

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```

cat gcg aaa aga acc tac aga gaa ctg cgg tta ctt aaa cat atg aaa 599
His Ala Lys Arg Thr Tyr Arg Glu Leu Arg Leu Leu Lys His Met Lys
              65              70              75

```

```

cat gaa aat gtg att ggt ctg ttg gac gtt ttt aca cct gca agg tct 647
His Glu Asn Val Ile Gly Leu Leu Asp Val Phe Thr Pro Ala Arg Ser
              80              85              90              95

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ctg gag gaa ttc aat gat gtg tat ctg gtg acc cat ctc atg ggg gca 695
Leu Glu Glu Phe Asn Asp Val Tyr Leu Val Thr His Leu Met Gly Ala
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gat ctg aac aac att gtg aaa tgt cag aag ctt aca gat gac cat gtt Asp Leu Asn Asn Ile Val Lys Cys Gln Lys Leu Thr Asp Asp His Val 115 120 125	743
cag ttc ctt atc tac caa att ctc cga ggt cta aag tat ata cat tca Gln Phe Leu Ile Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser 130 135 140	791
gct gac ata att cac agg gac cta aaa cct agt aat cta gct gtg aat Ala Asp Ile Ile His Arg Asp Leu Lys Pro Ser Asn Leu Ala Val Asn 145 150 155	839
gaa gac tgt gag ctg aag att ctg gat ttt gga ctg gct cgg cac aca Glu Asp Cys Glu Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg His Thr 160 165 170 175	887
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ccc ctt gac caa gaa gag atg gag tcc tga gcacctgggt tctgttctgt      1465
Pro Leu Asp Gln Glu Glu Met Glu Ser
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 Met Ser Gln
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gag agg ccc acg ttc tac cgg cag gag ctg aac aag acc atc tgg gag 286
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 5 10 15

gtg ccc gaa cga tac cag aac ctg tcc ccg gtg ggc tcg ggc gcc tat 334
 Val Pro Glu Arg Tyr Gln Asn Leu Ser Pro Val Gly Ser Gly Ala Tyr
 20 25 30 35

ggc tgc gtg tgt gct gct ttt gat aca aag acg ggg cat cgt gtg gca 382
 Gly Ser Val Cys Ala Ala Phe Asp Thr Lys Thr Gly His Arg Val Ala
 40 45 50

gtt aag aag ctg tgc aga ccg ttt cag tcc atc att cac gcc aaa agg 430
 Val Lys Lys Leu Ser Arg Pro Phe Gln Ser Ile Ile His Ala Lys Arg
 55 60 65

acc tac cga gag ttg cgt ctg ctg aag cac atg aaa cac gaa aat gtg 478
 Thr Tyr Arg Glu Leu Arg Leu Leu Lys His Met Lys His Glu Asn Val
 70 75 80

att ggt ctg ttg gat gtg ttc aca ccc gca agg tca ctg gag gaa ttc 526
 Ile Gly Leu Leu Asp Val Phe Thr Pro Ala Arg Ser Leu Glu Glu Phe
 85 90 95

aat gac gtg tac ctg gtg acc cat ctc atg ggg gcg gac ctg aac aac 574
 Asn Asp Val Tyr Leu Val Thr His Leu Met Gly Ala Asp Leu Asn Asn
 100 105 110 115

atc gtg aag tgc cag aag ctg acc gac gac cac gtt cag ttt ctc atc 622
 Ile Val Lys Cys Gln Lys Leu Thr Asp Asp His Val Gln Phe Leu Ile
 120 125 130

tac cag atc ctc cga ggg ctg aag tat ata cat tgc gct gac ata att 670
 Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asp Ile Ile
 135 140 145

cac agg gac cta aag ccc agc aac cta gct gtg aac gaa gac tgt gag 718
 His Arg Asp Leu Lys Pro Ser Asn Leu Ala Val Asn Glu Asp Cys Glu
 150 155 160

ctc aag att ctg gat ttt ggg ctg gct cgg cac act gat gat gag atg 766
 Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg His Thr Asp Asp Glu Met
 165 170 175

aca ggc tac gtg gct acc agg tgg tac cga gcc cca gag atc atg ctg 814
 Thr Gly Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Ile Met Leu
 180 185 190 195

aat tgg atg cac tat aac cag aca gtg gat att tgg tcc gtg ggc tgc 862
 Asn Trp Met His Tyr Asn Gln Thr Val Asp Ile Trp Ser Val Gly Cys
 200 205 210

atc atg gct gag ctg ttg acc gga aga acg ttg ttt cct ggt aca gac 910
 Ile Met Ala Glu Leu Leu Thr Gly Arg Thr Leu Phe Pro Gly Thr Asp
 215 220 225

cat att aac cag ctt cag cag ata atg cgt atg acg ggg aca ccc cct 958
 His Ile Asn Gln Leu Gln Gln Ile Met Arg Met Thr Gly Thr Pro Pro
 230 235 240

gct tat ctc att aac agg atg cca agc cat gag gca aga aac tac att 1006
 Ala Tyr Leu Ile Asn Arg Met Pro Ser His Glu Ala Arg Asn Tyr Ile
 245 250 255

cag tct ctg gcc cag atg ccg aag atg aac ttc gca aat gta ttt att 1054
 Gln Ser Leu Ala Gln Met Pro Lys Met Asn Phe Ala Asn Val Phe Ile
 260 265 270 275

ggt gcc aat ccc ctg gct gtc gac cta ctg gag aag atg ctc gtt ttg 1102
 Gly Ala Asn Pro Leu Ala Val Asp Leu Leu Glu Lys Met Leu Val Leu
 280 285 290

gac tca gat aag agg atc aca gca gcc caa gct ctt gcg cat gcc tac 1150
 Asp Ser Asp Lys Arg Ile Thr Ala Ala Gln Ala Leu Ala His Ala Tyr
 295 300 305

ttt gct cag tac cac gac cct gat gat gag cct gtt gct gac cct tat 1198
 Phe Ala Gln Tyr His Asp Pro Asp Asp Glu Pro Val Ala Asp Pro Tyr
 310 315 320

gac cag tcc ttt gaa agc agg gac ctt ctc ata gat gag tgg aag agc 1246
 Asp Gln Ser Phe Glu Ser Arg Asp Leu Leu Ile Asp Glu Trp Lys Ser
 325 330 335

ctg acc tat gat gaa gtc atc agc ttt gtg cca cca ccc ctt gac caa 1294
 Leu Thr Tyr Asp Glu Val Ile Ser Phe Val Pro Pro Pro Leu Asp Gln
 340 345 350 355

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 Glu Glu Met Glu Ser
 360

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 aagaactgtt tgcataatth tctgaattht gagcacttht tgctatataa ggaccatata 2842
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 cgaggacctt gaatcattht gagcccagaa ggaggcagac tggccaggtc tcaccacctc 3022
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 gaatgccaag tgtgatttht aacaattctg ctctgggtat ttcattgaag acatctthtgc 3142
 acatgtgacc atgtgtgtgt aggggctgtg ttccagggac tggactcgaa gctagaactg 3202
 gcagaagagt tctggcatcc acagcgcaat gctgccacca cccagtttct tcatcagaag 3262
 acaagggaac gagaaaactg ctgttcgttht gtatttgtga acttggtgt aatctggtat 3322
 gccataggat gtcagataat accactgggt 3352

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<211> 503
 <212> DNA
 <213> M. musculus

<400> 169
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 tcactaacac tactgaacat agtcattctg aaagtctgtg tttttacagg caagaaacta 180
 cattcagtct ctggcccag atg ccg aag atg aac ttc gca aat gta ttt att 232
 ggt gcc aat ccc ctg gct gtc gac cta ctg gag aag atg ctc gtt ttg 280
 gac tca gat aag agg atc aca gca gcc caa gct ctt gcg cat gct act 328
 ttg ctc agt acc acg acc ctg atg atg agc ctg ttg ctg acc ctt atg 376
 acc agt cct ttg aaa gca ggg acc ttc tca tag atgagtggaa gagcctgacc 429
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 gcacctgggt tctg 503

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 <213> M. musculus

<220>
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 <222> (297)...(1073)

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 gccgacgctc gtaggagccg ccgcggctga cagggggcggc gggctgcagc ctccacacct 180
 gcgcgggttg cgggcgcggg gtccgggtctg ccgcggggcgg gcgcagagga gagcgtgcgg 240
 ctgcaggcag gagccccgc tcggccacct cctcgccccg ctgctgccgc tggaag atg 299
 Met
 1
 tcg cag gag agg ccc acg ttc tac cgg cag gag ctg aac aag acc atc 347
 Ser Gln Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys Thr Ile
 5 10 15
 tgg gag gtg ccc gaa cga tac cag aac ctg tcc ccg gtg ggc tcg ggc 395
 Trp Glu Val Pro Glu Arg Tyr Gln Asn Leu Ser Pro Val Gly Ser Gly
 20 25 30
 gcc tat ggc tcg gtg tgt gct gct ttt gat aca aag acg ggg cat cgt 443
 Ala Tyr Gly Ser Val Cys Ala Ala Phe Asp Thr Lys Thr Gly His Arg
 35 40 45
 gtg gca gtt aag aag ctg tcg aga ccg ttt cag tcc atc att cac gcc 491
 Val Ala Val Lys Lys Leu Ser Arg Pro Phe Gln Ser Ile Ile His Ala
 50 55 60 65
 aaa agg acc tac cga gag ttg cgt ctg ctg aag cac atg aaa cac gaa 539
 Lys Arg Thr Tyr Arg Glu Leu Arg Leu Leu Lys His Met Lys His Glu
 70 75 80
 aat gtg att ggt ctg ttg gat gtg ttc aca ccc gca agg tca ctg gag 587
 Asn Val Ile Gly Leu Leu Asp Val Phe Thr Pro Ala Arg Ser Leu Glu
 85 90 95
 gaa ttc aat gac gtg tac ctg gtg acc cat ctc atg ggg gcg gac ctg 635
 Glu Phe Asn Asp Val Tyr Leu Val Thr His Leu Met Gly Ala Asp Leu

100	105	110	
aac aac atc gtg aag tgc cag aag ctg acc gac gac cac gtt cag ttt			683
Asn Asn Ile Val Lys Cys Gln Lys Leu Thr Asp Asp His Val Gln Phe			
115	120	125	
ctc atc tac cag atc ctc cga ggg ctg aag tat ata cat tcg gct gac			731
Leu Ile Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asp			
130	135	140	145
ata att cac agg gac cta aag ccc agc aac cta gct gtg aac gaa gac			779
Ile Ile His Arg Asp Leu Lys Pro Ser Asn Leu Ala Val Asn Glu Asp			
	150	155	160
tgt gag ctc aag att ctg gat ttt ggg ctg gct cgg cac act gat gat			827
Cys Glu Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg His Thr Asp Asp			
	165	170	175
gag atg aca ggc tac gtg gct acc agg tgg tac cga gcc cca gag atc			875
Glu Met Thr Gly Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Ile			
	180	185	190
atg ctg aat tgg atg cac tat aac cag aca gtg gat att tgg tcc gtg			923
Met Leu Asn Trp Met His Tyr Asn Gln Thr Val Asp Ile Trp Ser Val			
	195	200	205
ggc tgc atc atg gct gag ctg ttg acc gga aga acg ttg ttt cct ggt			971
Gly Cys Ile Met Ala Glu Leu Leu Thr Gly Arg Thr Leu Phe Pro Gly			
210	215	220	225
aca gac cat att gat cag ttg aag ctc att tta aga ctc gtt gga acc			1019
Thr Asp His Ile Asp Gln Leu Lys Leu Ile Leu Arg Leu Val Gly Thr			
	230	235	240
cca ggg gct gag ctt ctg aag aaa atc tcc tca gag tct gat gcc aag			1067
Pro Gly Ala Glu Leu Leu Lys Lys Ile Ser Ser Glu Ser Asp Ala Lys			
	245	250	255
cca tga ggtgagaaca aacagcatgc acaggggaagt ctacctcgga ggccaccttc			1123
Pro			
tcgtagtagt gtctgtgtat agccagcagt ttctaattgtc accgaatgct tgcattgtgcc			1183
ccaagaaccg ttaaagcagt actggctgtg tgctagcggg gtgttggcat ttaggatgca			1243
gtctcctgag cctgcgagggc agcgatgcag tgtagggcag tgttccttag tgtttggctt			1303
tctgatcttg tgcttgaggt aacaagtgtc gttgcagttg tatgtagtta ggggtgtgcta			1363
cagccgtgtc atgggtgcat ggaacagagt tcattagtgt gctttgctct ccacccattt			1423
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aaaaaaaaa aaaaaaa			1500
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ttgatacaaa gacggggcat cgtgtggcag ttaagaagct gtcgagaccg tttcagtcca			180
tcattcacgc caaaaggacc taccgagagt tgcgtctgct gaagcacatg aaacacgaaa			240

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atgtgattgg tctgttggat gtgttcacac ccgcaaggct actggaggaa ttcaatgacg 300
tgtacctggg gacccatctc atgggggcgg acctgaacaa catcgtgaag tgccagaagc 360
tgaccgacga ccacgttcag tttc                                     384

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<210> 172

<211> 463

<212> DNA

<213> M. musculus

<220>

<221> misc_feature

<222> 429

<223> n = A, T, C, or G

<400> 172

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tgaagcgcga gcgggtgtct tgccggcgtc gcgtgcgctc cctccccggg gaggcggctgc 180
aggaggaccg cggcggggagc agcctcgagc cgtgcagccg gctccggcac cttgccgacg 240
ctcgtaggag ccgcgcgcgc tgacaggggc ggccgggtcgc accctccaca cctgcgcggg 300
tgccgggcgc ggggtccggg ctgccgcggg cgggcgcaga ggagagcgtg cggctgcagg 360
caggagcccc cgctcggcca cctcctcgcc ccgctgctgc cgctggaaga tgtcgcagga 420
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<210> 173

<211> 1083

<212> DNA

<213> R. norvegicus

<220>

<221> CDS

<222> (1)...(1083)

<400> 173

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Met Ser Gln Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys Thr
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gtc tgg gag gtg ccc gag cga tac cag aac ctg tcc ccg gtg ggc tcg 96
Val Trp Glu Val Pro Glu Arg Tyr Gln Asn Leu Ser Pro Val Gly Ser
          20          25          30

gga gcc tac ggc tcg gtg tgt gct gct ttt gat aca aag acg gga cat 144
Gly Ala Tyr Gly Ser Val Cys Ala Ala Phe Asp Thr Lys Thr Gly His
          35          40          45

cgt gtg gca gtg aag aag ctg tcg aga ccg gtt cag ccc atc att cac 192
Arg Val Ala Val Lys Lys Leu Ser Arg Pro Val Gln Pro Ile Ile His
          50          55          60

gcc aaa agg tcc tac agg gag ctg cgg ctg ctg aag cac atg aag cac 240
Ala Lys Arg Ser Tyr Arg Glu Leu Arg Leu Leu Lys His Met Lys His
          65          70          75          80

gag aat gtg att ggt ctg ttg gat gtg ttt aca cct gca agg tcc ctg 288
Glu Asn Val Ile Gly Leu Leu Asp Val Phe Thr Pro Ala Arg Ser Leu
          85          90          95

gag gaa ttc aac gat gtg tac ctg gtg acc cat ctc atg ggg gca gac 336

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Glu Glu Phe Asn Asp Val Tyr Leu Val Thr His Leu Met Gly Ala Asp	
100 105 110	
ctg aac aac atc gtg aag tgt cag aag ctt acc gat gac cac gtt cag	384
Leu Asn Asn Ile Val Lys Cys Gln Lys Leu Thr Asp Asp His Val Gln	
115 120 125	
ttt ctt atc tac cag atc ctg cga ggg ctg aag tat ata cac tcg gct	432
Phe Leu Ile Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala	
130 135 140	
gac ata atc cac agg gac cta aag ccc agc aac ctc gct gtg aat gaa	480
Asp Ile Ile His Arg Asp Leu Lys Pro Ser Asn Leu Ala Val Asn Glu	
145 150 155 160	
gac tgt gag ctg aag att ctg gat ttt ggg ctg gct cgg cac act gat	528
Asp Cys Glu Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg His Thr Asp	
165 170 175	
gac gaa atg acc ggc tac gtg gct acc cgg tgg tac aga gcc ccc gag	576
Asp Glu Met Thr Gly Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu	
180 185 190	
att atg ctg aat tgg atg cac tac aac cag aca gtg gat att tgg tcc	624
Ile Met Leu Asn Trp Met His Tyr Asn Gln Thr Val Asp Ile Trp Ser	
195 200 205	
gtg ggc tgc atc atg gct gag ctg ttg acc gga aga acg ttg ttt cct	672
Val Gly Cys Ile Met Ala Glu Leu Leu Thr Gly Arg Thr Leu Phe Pro	
210 215 220	
ggg aca gac cat att gat cag ttg aag ctc att tta aga ctc gtt gga	720
Gly Thr Asp His Ile Asp Gln Leu Lys Leu Ile Leu Arg Leu Val Gly	
225 230 235 240	
acc cca ggg gct gag ctt ctg aag aaa atc tcc tca gag tct gca aga	768
Thr Pro Gly Ala Glu Leu Leu Lys Lys Ile Ser Ser Glu Ser Ala Arg	
245 250 255	
aac tac att cag tct ctg gcc cag atg ccg aag atg aac ttc gca aat	816
Asn Tyr Ile Gln Ser Leu Ala Gln Met Pro Lys Met Asn Phe Ala Asn	
260 265 270	
gta ttt att ggt gcc aat ccc ctg gct gtc gac ctg ctg gaa aag atg	864
Val Phe Ile Gly Ala Asn Pro Leu Ala Val Asp Leu Leu Glu Lys Met	
275 280 285	
ctg gtt ttg gac tca gat aag agg atc aca gca gcc caa gct ctt gcg	912
Leu Val Leu Asp Ser Asp Lys Arg Ile Thr Ala Ala Gln Ala Leu Ala	
290 295 300	
cat gcc tac ttt gct cag tac cac gac cct gat gat gag cca gtg gct	960
His Ala Tyr Phe Ala Gln Tyr His Asp Pro Asp Asp Glu Pro Val Ala	
305 310 315 320	
gac cct tat gac cag tcc ttt gaa agc agg gac ctc ctt ata gac gaa	1008
Asp Pro Tyr Asp Gln Ser Phe Glu Ser Arg Asp Leu Leu Ile Asp Glu	
325 330 335	
tgg aag agc ctg acc tac gat gaa gtc att agc ttt gtg cca ccg ccc	1056
Trp Lys Ser Leu Thr Tyr Asp Glu Val Ile Ser Phe Val Pro Pro Pro	

340 345 350 1083

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Leu Asp Gln Glu Glu Met Asp Ser
355 360

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<220>
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<210> 175
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ctgcgacatt ttccagcggc 20

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catcatcagg gtcgtggtac 20

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aggtgctcag gactccatct 20

<210> 178
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<210> 184
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<400> 184
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<400> 185
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<210> 187
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<210> 194

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<210> 195

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Antisense Oligonucleotide

<400> 195

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<210> 196

<211> 20

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<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

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<210> 197

<211> 20

<212> DNA

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<223> Antisense Oligonucleotide

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<210> 198

<211> 20

<212> DNA

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<220>

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<210> 199
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<210> 200
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<210> 201
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<210> 203
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